Toward Patient-Specific Mapping of Early Corneal Alterations

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Abstract

A methodology for patient-specific corneal cone demarcation based on spatially resolved tissue analysis from Scheimpflug images is presented. Tissue-derived maps revealed localized corneal abnormalities not identifiable in conventional tomographic maps, particularly in subclinical keratoconus, enabling earlier spatial characterization of ectatic changes.

Introduction

Corneal ectatic diseases, such as keratoconus (KC), are characterized by a progressive localized deformation of the cornea, typically leading to a cone-like shape. Accurate identification and spatial characterization of this cone are essential for disease management and treatment planning, yet precise patient-specific cone demarcation remains clinically unavailable.

Early detection of ectatic corneal diseases is critical to avoid severe visual deterioration and to reduce the risk of postoperative ectasia following refractive surgery. Beyond diagnosis, cone demarcation also has therapeutic implications. Current corneal cross-linking (CXL) surgery is typically applied over the whole corneal despite the highly localized nature of ectatic changes. A patient-specific identification of the ectatic area could therefore contribute to more personalized and localized treatment strategies.

The purpose of this work was to present a methodology for cone demarcation based on tissue-derived information extracted from Scheimpflug images, potentially enabling the identification of localized ectatic regions before clinically detectable shape abnormalities become evident.

Methodology

A total of 10 control eyes, 10 subclinical KC eyes, and 10 KC eyes were included in this study. Conventional corneal shape maps for each eye were exported directly from the Pentacam HR device (Oculus, Germany), including curvature- and pachymetry-based descriptors.

In parallel, tissue-derived maps were generated from the Scheimpflug images following a previously described methodology [1] illustrated in Figure 1. Briefly, the 25 Scheimpflug meridians acquired by the Pentacam HR rotating camera (Figure 1a), were individually segmented to isolate the cornea [2]. A moving region of interest (ROI) was then sequentially displaced along the corneal tissue in each image to locally analyze the pixel intensity distribution (Figure 1b). The moving ROI covered approximately the central 7 mm of the cornea.

For every ROI, the corresponding pixel intensity distribution was fitted using a Weibull probability density function, obtaining spatially resolved tissue-related parameters (shape and scale). In particular, the scale parameter, related to tissue transparency, has previously shown special relevance for the detection of subclinical KC [1], and was further analysed. The parameter values from all meridians (Figure 1c) were subsequently transformed from Cartesian into polar coordinates, interpolated, and smoothed using second-order Zernike polynomials to reconstruct two-dimensional corneal tissue maps (Figure 1d).

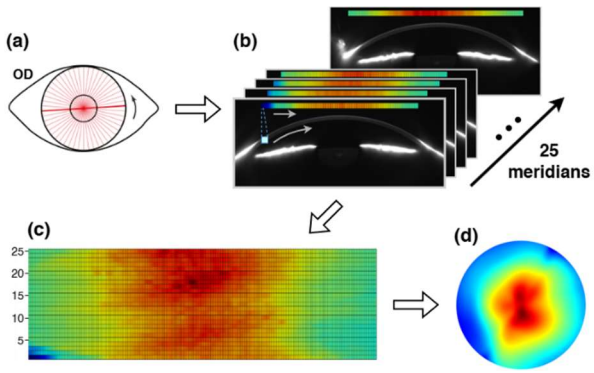

Figure 1. Main steps to obtain corneal tissue maps from each Scheimpflug measurement.

The coordinates of the tissue-derived maps and the conventional tomographic maps were spatially matched to ensure point-to-point correspondence across modalities. Cone demarcation was then performed on the tissue-derived maps using a second-order Fourier series representation of the abnormal region contour, defined by a fixed empirically determined threshold that was kept constant across all eyes. Finally, the resulting cone boundary was transferred onto the conventional shape-based maps to enable direct spatial comparison between tissue-derived and tomographic abnormalities.

Results

Representative corneal tissue maps derived from the scale parameter for the three study groups are shown in Figure 2. Control eyes presented a homogeneous spatial distribution without detectable abnormal contour regions, whereas subclinical KC and KC eyes showed progressively more localized contour-defined tissue abnormalities.

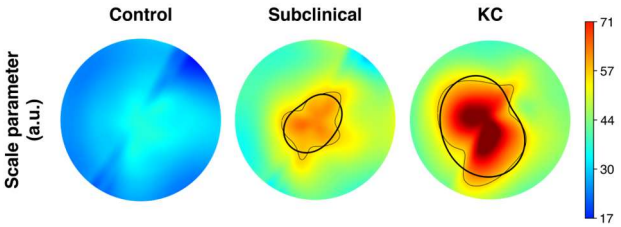

Figure 2. Representative tissue-derived maps from the scale parameter of pixel intensity distribution modelled with a Weibull distribution for control, subclinical KC, and KC eyes. Thin contours indicate the empirically defined abnormal region used for cone demarcation, and thick contours show the corresponding second-order Fourier approximation. Note that no cone was demarcated in the control eye because the predefined threshold was not reached.

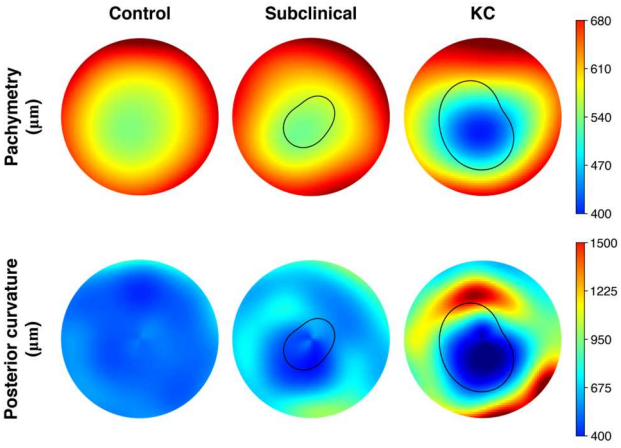

Figure 3. Representative conventional tomographic maps with projected tissue-derived cone boundaries for each study group. First row: pachymetry maps. Second row: posterior curvature maps.

The transfer of the tissue-derived cone boundaries onto conventional tomographic maps is illustrated in Figure 3. In KC eyes, the fitted boundaries showed a clear spatial correspondence with regions of reduced pachymetry and reduced posterior curvature. In subclinical KC eyes, conventional tomographic maps were very similar to those of control eyes, with no clearly identifiable ectatic region, despite tissue-derived maps already revealing localized differences. This trend was consistently observed across the remainder of the dataset.

Conclusions

This study presents a methodology for corneal cone demarcation based on tissue-derived information extracted from Scheimpflug images. The proposed approach enables the identification and spatial characterization of localized corneal alterations, which are not fully captured by conventional tomographic maps, particularly in subclinical KC cases.

The results suggest a consistent spatial agreement between tissue-derived cone boundaries and tomographic abnormalities in KC eyes, while subclinical cases show earlier localized tissue changes that are not yet clearly reflected in standard corneal shape descriptors. These findings support the potential value of tissue-based maps for improving the spatial characterization of ectatic processes.

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